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      Li, Jing  
      Nishizawa, Kazuhisa  
      Wagner, Gerhard
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<130> 1062.1021-004

<151> 1998-12-04

<151> 1999-01-13

<151> 1999-11-15

<160> 25

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<170> FastSEQ for Windows Version 4.0
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 $\langle 210 \rangle$ 1

<211> 1299

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

 $\langle 222 \rangle \quad (121) \dots (1143)$

<400> 1

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 atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gag gat 168
 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
 1 5 10 15

gag gat gaa atc att gtc ccc aag aag aag ctg gtg gac cct gtg gct 216
Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
20 25 30

ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264
Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
35 40 45

agc gat gag gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac 312
 Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
 50 55 60

atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc 360
Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
65 70 75 80

1032

cag acc tgg gtg agt gaa ggc tac ttc ccg gac ggt gtt tat tgc cgg 1080
 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
 305 310 315 320

aag ctg gac ccc cct ggt ggt cag ttc tac aac tcc aaa cgc att gac 1128
 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
 325 330 335

ttt gac ctc tac acc tgagcctgct gggggccag tttggtgggc ccttctttcc 1183
 Phe Asp Leu Tyr Thr
 340

tggaactttgt ggaggaggca ccaagtgtct caggcagcga ggaaattgga ggccattttt 1243
 cagtcaattt ccctttccca ataaaagcct tagttgtgta aaaaaaaaaa aaaaaa 1299

<210> 2
 <211> 341
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
 1 5 10 15
 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
 20 25 30
 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
 35 40 45
 Ser Asp Glu Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
 50 55 60
 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
 65 70 75 80
 Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
 85 90 95
 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp
 100 105 110
 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile
 115 120 125
 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu
 130 135 140
 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly
 145 150 155 160
 Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
 165 170 175
 Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
 180 185 190
 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln
 195 200 205
 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg
 210 215 220
 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
 225 230 235 240
 Asn Pro Thr Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
 245 250 255
 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu
 260 265 270
 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
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<210> 7
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<400> 7

<210> 8

<211> 27

<212> PRT

<400> 8

<210> 9

<211> 17

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Motif in CD2 binding region of CD2BP2

<221> VARIANT

<222> (1) ... (2)

<223> Xaa = Any Amino Acid

<221> VARIANT

$\langle 222 \rangle \quad (3) \dots (3)$

<223> Xaa can be Tyr or Phe

<221> VARIANT

<222> (4) . . . (7)

<223> Xaa = Any Amino Acid

<221> VARIANT

$$\langle 222 \rangle \quad (8) \dots (8)$$

<223> Xaa can be Met or Val

<221> VARIANT

<222> (9) ... (15)

<223> Xaa = Any Amino Acid

<400> 9

<210> 10

<211> 6

<212> PRT
 <213> Artificial Sequence
 <220>
 <223> CD2BP2 binding region

<400> 10
 Pro Pro Pro Gly His Arg
 1 5

<210> 11
 <211> 70
 <212> PRT
 <213> Homo sapiens

<400> 11
 Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro
 1 5 10 15
 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro
 20 25 30
 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro
 35 40 45
 Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser
 50 55 60
 Leu Ser Pro Ser Ser Asn
 65 70

<210> 12
 <211> 8
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Kozak consensus sequence

<400> 12
 ccgccacc

8

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Flag Epitope

<400> 13
 gactacaagg acgacgatga caag

24

<210> 14
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Flag Epitope

<400> 14
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 15
 <211> 31
 <212> PRT
 <213> Gallus gallus

<220>
 <223> Flag Epitope

<400> 15
 Trp Tyr Tyr Lys Asp Pro Gln Gly Glu Ile Gln Gly Pro Phe Ser Asn
 1 5 10 15
 Gln Glu Met Ala Glu Trp Phe Gln Ala Gly Tyr Phe Thr Met Ser
 20 25 30

<210> 16
 <211> 38
 <212> PRT
 <213> Drosophila melanogaster

<220>
 <223> Flag Epitope

<400> 16
 Glu Val Thr Trp Glu Phe Lys Trp Ser Gln Asp Glu Thr Asp Ile Gln
 1 5 10 15
 Gly Pro Phe Ser Thr Glu Lys Met Leu Lys Trp Ser Gln Glu Asn Thr
 20 25 30
 Arg Tyr Phe Lys Asn Gly
 35

<210> 17
 <211> 34
 <212> PRT
 <213> Leishmania major

<220>
 <223> Flag Epitope

<400> 17
 Val Trp Met Met Arg Trp Lys Ala Lys Pro Thr Val Gln His Gly Pro
 1 5 10 15
 Phe Thr Asp Asp Ala Ile Gln Gln Trp Gly Arg Asp Gly Tyr Phe Gly
 20 25 30
 Lys Lys

<210> 18
 <211> 36
 <212> PRT
 <213> Caenorhabditis elegans

<220>

<223> Flag Epitope

<400> 18

Val	Ile	Asp	Thr	Lys	Trp	His	Tyr	Leu	Gly	Pro	Asp	Ser	Glu	Lys	Tyr
1				5					10					15	
Gly	Pro	Tyr	Met	Ser	Lys	Asp	Met	Leu	Phe	Trp	Leu	Gln	Ala	Gly	Tyr
			20					25					30		
Phe	Asn	Asp	Gly												
			35												

<210> 19

<211> 35

<212> PRT

<213> *Caenorhabditis elegans*

<220>

<223> Flag Epitope

<400> 19

Val	Glu	Ser	Ser	Trp	Arg	Tyr	Ile	Asp	Thr	Gln	Gly	Gln	Ile	His	Gly
1				5					10					15	
Pro	Phe	Thr	Ile	Gln	Met	Met	Ser	Gln	Trp	Tyr	Ile	Gly	Gly	Tyr	Phe
			20					25					30		
Ala	Ser	Thr													
			35												

<210> 20

<211> 35

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<223> Flag Epitope

<400> 20

Ile	Glu	Ser	Gln	Trp	Lys	Tyr	Ile	Asp	Ser	Asn	Gly	Asn	Ile	Gln	Gly
1				5					10					15	
Pro	Phe	Gly	Thr	Asn	Asn	Met	Ser	Gln	Trp	Tyr	Gln	Gly	Gly	Tyr	Phe
			20					25					30		
Thr	Pro	Thr													
			35												

<210> 21

<211> 31

<212> PRT

<213> *Saccharomces pombe*

<220>

<223> Flag Epitope

<400> 21

Trp	Leu	Tyr	Lys	Asp	Pro	Gln	Asn	Asn	Val	Gln	Gly	Pro	Phe	Thr	Gly
1				5					10					15	
Val	Asp	Met	His	Gln	Trp	Tyr	Arg	Ala	Gly	Tyr	Phe	Pro	Leu	Gly	
			20					25					30		

<210> 22
 <211> 21
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Flag Epitope

<400> 22
 Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro
 1 5 10 15
 Pro Pro Gly His Arg
 20

<210> 23
 <211> 62
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Flag Epitope

<400> 23
 Asp Val Met Trp Glu Tyr Lys Trp Glu Asn Thr Gly Asp Ala Glu Leu
 1 5 10 15
 Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr Trp Val Ser Glu Gly
 20 25 30
 Tyr Phe Pro Asp Gly Val Tyr Cys Arg Lys Leu Asp Pro Gly Gly
 35 40 45
 Gln Phe Tyr Asn Ser Lys Arg Ile Asp Phe Asp Leu Tyr Thr
 50 55 60

<210> 24
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Flag Epitope

<400> 24
 Trp Tyr Tyr Lys Asp Pro Gln Gly Glu Ile Gln Gly Pro Phe Asn Asn
 1 5 10 15
 Gln Glu Met Ala Glu Trp Phe Gln Ala Gly Tyr Phe Thr Met Ser
 20 25 30

<210> 25
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Flag Epitope

<400> 25

10/10

Gln	Trp	Phe	Ser	Arg	Ser	Leu	Ala	Pro	Cys	Pro	Gly	Pro	Phe	Thr	Thr
1				5					10					15	
Gln	Glu	Met	Ala	Glu	Trp	Phe	Gln	Ala	Gly	Tyr	Phe	Ser	Met	Ser	
			20				25						30		

[illegible]